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(57) Abstract

T-cell epitopes of or derived from the TraT protein of *E. coli* have been identified and used in the preparation of complexes with immunogens to enhance or provide immune responses to the immunogens. The complexes can be prepared either directly, by chemical linkage or as fusion proteins. Where the complexes are prepared as fusion proteins the invention provides for polynucleotides encoding the fusion proteins as well as transformant hosts capable of expressing the fusion proteins. The fusion proteins may be expressed either intracellularly or exported to and expressed on the surface of the transformant host.

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T-Cell Epitopes

Technical Field

The present invention relates to isolated or synthetic sequences of or derived from TraT (a protein molecule isolated from the outer-membrane of certain strains of Escherichia coli) which function as T-cell epitopes. Such sequences can be employed in the preparation of vaccines which involve the use of carrier peptides to enhance antibody production to an immunogen and/or stimulate strong cell-mediated immunity to the immunogen whilst avoiding the use of larger carrier protein molecules.

Background Art

The generation of an immune response against a pathogen (bacterial, viral or parasite) depends, in the first instance, on the delivery of the appropriate stimulus to the immune system of the host. The pathogen or infectious agent presents the host with a number of immune-stimulating compounds or antigens which are usually large molecules such as proteins, polysaccharides or glycoproteins. These antigens may provoke one or more different types of reaction from the host in an effort to destroy or eliminate the invading organism. Accordingly, the antigen may stimulate T-cells which provide cell-mediated immunity and/or an antigen may stimulate B cells to initiate the synthesis and secretion of antibody (humoral immunity). The development and maintenance of the individual's protective immune response to a foreign antigen is usually dependent on achieving a critical level of stimulation of both cell-mediated and humoral immunity.

In the generation of a protective immune response, a certain type of T-cell, a helper T-cell is frequently required to assist the B-cell to grow and secrete soluble antibody. These helper T-cells also interact with and recognize antigens on the surface of antigen-presenting cells such as macrophages and, by releasing soluble

factors (cytokines), mediate activation and differentiation of B-cells.

Certain small molecules termed haptens, of which short peptides are an example, are usually poorly immunogenic while larger molecules such as proteins and some polysaccharides are usually immunogenic in that they elicit a satisfactory protective response. To obviate the problems of inducing immunity to poorly immunogenic molecules, attempts have been made to enhance their immunogenicity by binding them to "carrier" molecules. These carriers, which are usually immunogenic proteins, function by stimulating the T-cell co-operative effect that occurs with naturally immunogenic molecules. That is to say, a poorly immunogenic antigen, bound to a carrier, will elicit T-cell help in antibody production. By engaging the T-cells with carrier determinants, B-cells will begin antibody production not only to the carrier itself, but also to the bound antigenic determinant.

Although it is widely accepted that the carrier principle is an effective method of improving the efficacy of vaccines, the number of proteins which are ethically accepted for use as potential carrier proteins for human use is relatively limited. These include tetanus toxoid and diphtheria toxoid. The limited number of available carrier proteins means that a large number of vaccine products will employ one of these proteins and multiple immunizations with products conjugated to these carriers increases the possibility that undesirable reactions to these carriers will occur. Also, these carriers have been chosen in the first instance, not for their immunostimulatory characteristics, but rather because they were already registered for human use. It is clear, therefore, that there is a need for an alternative carrier to those currently used in conjugate vaccines which will obviate the immunological problems associated with these vaccines and yet retain the same immunogenicity as the vaccines presently in use or improve on it.

During the past decade it has become clear that certain fragments of proteins, rather than the entire protein molecule, are preferentially recognized by T-cells in association with an appropriate self (Class I or Class II) antigen. These fragments are known as T-cell epitopes and their co-recognition (i.e., in association with certain Class I or Class II molecules) by T-cells ensures the delivery of "T-cell help" so that a B cell can be activated and undergo differentiation to secrete antibody.

It is generally accepted that T-cell recognition of proteins is more complex than antibody binding, and, despite recent advances in our understanding of T-cell epitopes, less clearly understood. However, in the mid 1980s it was suggested that T-cell determinants (epitopes) have a tendency to form stable helical structures in which the hydrophilic groups align on one surface of the helix while hydrophobic residues align on the opposing surface. In this model, it is proposed that the hydrophobic surface would normally be found associated with the MHC antigen while the more hydrophilic surface would be exposed to the T-cell receptor. Accordingly, an algorithm to search a given protein sequence for regions with a tendency to form helical amphipathic structures has been developed and applied to several protein models (De Lisi and Berzofsky, P N A S 82: 7048, 1985). In contrast, some workers maintain that T-cell determinants are associated with beta turns within the protein. However, these algorithms frequently fail to detect T-cell epitopes and conversely often select sequences which do not function as T-cell epitopes. In addition, these algorithms can not be used to define the strength or cross-species functionality of selected sequences. A unifying hypothesis of what factors are important for predicting T-cell epitopes has yet to emerge and the identification of such epitopes as well as the determination of their strength is still very much an empirical exercise. Although it is still not clear what a

T-cell perceives, there is agreement among several groups using a variety of models that a region of 7-17 amino acid residues in length is required for recognition.

T-cell epitopes from diphtheria toxin, tetanus toxin and cross-reacting material of diphtheria toxin were described in PCT/US89/00388. They differ from the T-cell epitopes of this invention.

Previous work (PCT/AU87/00107) has examined a number of integral membrane proteins for their ability to generate serum antibody responses in the absence of adjuvant. These proteins, which include TraT, have been shown to stimulate high titres of serum antibody in mice, rats, guinea-pigs and rabbits. The antibody titres elicited by injecting TraT in saline is not significantly increased by the addition of oil-based adjuvants such as Freund's Incomplete Adjuvant (FIA) or Montanide/Marcol. Covalent attachment of Bovine Serum Albumin or of the dinitrophenyl group or of a peptide antigen to TraT results in a significant enhancement of the immune response to the conjugated material as compared with the response seen when the immunogen is injected without adjuvant or not conjugated to TraT. The antibody response to these conjugates is not significantly increased by the addition of FIA. TraT is a self-adjuvanting carrier molecule which is capable of generating high antibody titres to itself as well as to molecules attached to it.

Abbreviations

AlOH - aluminium hydroxide
CPM - counts per minute
DEAE - diethylaminoethyl
DMF -dimethyl formamide
DT - diphtheria toxoid
EDTA - ethylene diamine tetraacetic acid
FIA - Freund's incomplete adjuvant
HPLC - High performance liquid chromatography
FCS - Foetal calf serum
LAL assay -Limulus Amoebocyte Lysate Assay
LHRH - Luteinizing hormone releasing hormone

LIP	- Liposome
LPS	- Lipopolysaccharide
MBS	- m-maleimido benzoic acid n-hydroxysuccinimide ester
PBS	- Phosphate buffered saline
PHA	- Phytohaemagglutinin
PMSF	- Phenylmethyl sulphonyl fluoride
QA	- Quality assurance
QC	- Quality control
RPMI	- tissue culture medium
RT	- Room temperature
SAP	- Saponin
SDS	- Sodium dodecyl sulphate
SDS-PAGE	- Sodium dodecyl sulphate polyacrylamide gel electrophoresis
TFA	- Trifluoroacetic acid
VYDAC	- Trade name of chromatography column
ZWIT	- Zwittergent

Description of the Invention

According to the present invention isolated peptide sequences of or derived from TraT that by themselves have unexpectedly high immunostimulatory properties in a range of species have been identified and used. The specific sequences T1, T2, T4 and T6 (SEQUENCE ID Nos 1, 2, 4, and 6 respectively) described herein are recognized by several phylogenetically diverse species, including primates.

To the knowledge of the present inventors, T-cell stimulating peptide sequences that cross several species barriers have not been reported previously.

The finding that TraT (SEQUENCE ID No. 16) was a strong self-adjuvanting carrier molecule led the present inventors to consider that there might be particular peptide sequences within this protein which are preferentially recognized by T-cells. As a result of scanning the TraT molecule and considering factors which might enhance activity as a T-cell epitope, seven peptides

derived from the TraT molecule were synthesized and then tested in T-cell proliferative assays using T-cells from a variety of animals that had been immunized with the native TraT molecule in saline. A hierarchical pattern of responsiveness to the peptides was observed in the four animal species studied and in particular four of the peptides (T1,T2, T4, T6: SEQUENCE ID Nos 1, 2, 4 and 6 respectivley) showed very strong responses in all four species tested. Because these peptide sequences cross several species barriers it is possible that they are recognized by T-cells both within and across species.

The amino acid sequences of the seven molecules are:

T1: GlyAlaMetSerThrAlaIleLysLysArgAsnLeuGluValLysThrGln MetSerGluThrIleTrpLeuGlu (SEQUENCE ID NO. 1)

T2: GlyLeuGlnGlyLysIleAlaAspAlaValLysAlaLysGly (SEQUENCE ID No. 2)

T3: SerGlnTrpLeuAsnArgGlyTyrGluGlyAlaAlaValGlyAlaAlaLeu GlyAlaGlyIleThrGly (SEQUENCE ID No. 3)

T4: GlyLeuAlaAlaGlyLeuValGlyMetAlaAlaAspAlaMetValGluAsp ValAsn (SEQUENCE ID No. 4)

T5: AspValGlnIleAlaGluArgThrLysAlaThrValThrThrAspAsnVal AlaAlaLeuArgGln (SEQUENCE ID No. 5)

T6: SerThrGluThrGlyAsnGlnHisHisTyrGlnThrArgValValSerAsn AlaAsnLys (SEQUENCE ID No. 6)

T7: LysValAsnLeuLysThrGluGluAlaLysProValLeuGluAspGlnLeu AlaLys (SEQUENCE ID No. 7)

The TraT sequences which correspond to these molecules are shown in Figure 5 and are as follows:

TraT(T1) GlyAlaMetSerThrAlaIleLysLysArgAsnLeuGluValLysThr GlnMetSerGluThrIleTrpLeuGlu (SEQUENCE ID No. 1)

TraT(T2) GlyLeuGlnGlyLysIleAlaAspAlaValLysAlaLysGly (SEQUENCE ID No. 2)

TraT(T3) GluSerGlnGlyTrpLeuAsnArgGlyTyrGluGlyAlaAlaValGly AlaAlaLeuGlyAlaGlyIleThrGly (SEQUENCE ID No.23)

TraT(T4) GlyLeuAlaAlaGlyLeuValGlyMetAlaAlaAspAlaMetValGlu AspValAsn (SEQUENCE ID No. 4)

TraT(T5) AspValGlnIleAlaGluArgThrLysAlaThrValThrThrAspAsn ValAlaAlaLeuArgGln (SEQUENCE ID No. 5)

TraT(T6) SerThrGluThrGlyAsnGlnHisLysTyrGlnThrArgValValSer AsnAlaAsnLys (SEQUENCE ID No. 24)

TraT(T7) LysValAsnLeuLysPheGluGluAlaLysProValLeuGluAspGln LeuAlaLys (SEQUENCE ID No. 25)

T1, T2, T4 and T5 are identical to the sequences which appear in the native TraT sequence. T3, T6 and T7 are modified compared with TraT(T3), TraT(T6) and TraT(T7). In T3 the amino terminal 4 residues GluSerGlnGly of TraT(T3) are replaced by SerGln. In T6, the Lys residue from position 9 of TraT(T6) is replaced by His. In T7, the Phe residue from position 6 of TraT(T7) is replaced by Thr. These alterations to the native sequences were made to enhance the T-cell epitope activity of these peptides.

According to a first embodiment of the present invention, there is provided a T-cell epitope comprising a portion of the amino acid sequence of the protein, TraT.

Typically the T-cell epitope is effective across species.

Specific T-cell epitopes according to the present invention include portions of TraT having T-cell epitope activity or derivatives thereof, such as T1, T2, T4 and T6 (SEQUENCE ID Nos 1, 2, 4 and 6) which have sequences as described above.

Each of the T-cell epitopes of the invention may be modified. Modifications in accordance with the present invention include the addition of an N-terminal pyro-glutamic acid residue, the substitution of an N-terminal glutamic acid residue by a pyroglutamic acid residue and/or the addition or substitiution of a C-terminal cysteinamide as well as the specific modifications made in T3, T6 and T7 and described above. Modified T-cell epitopes of the invention fall within the scope of the present invention and are included within the term "T-cell epitope" when used herein as appropriate, and are included in references to particular T-cell epitopes of the invention as appropriate. In the preparation of fusion proteins of the invention modifications to the epitope to alter internal amino acids or terminal residues may be made posttranslationally or in the coding sequence as appropriate. The modifications should conserve the T-cell epitope activity of the parent molecule.

The invention also provides a complex comprising at least one T-cell epitope of the first embodiment linked to at least one immunogen wherein the immunogen and the epitope are linked such that the at least one T-cell epitope can still function as a T-cell epitope and the at least one immunogen still presents at least one antigenic determinant against which an immune response can be raised.

The invention further provides a vaccine comprising a complex of the invention together with a pharmaceutically acceptable carrier, excipient, diluent and/or adjuvant.

The complexes of the invention may be prepared by a number of routes. They may be prepared directly or by chemical coupling using appropriate linking or coupling agents or by modification of residues to provide sites for linkage. They may also be prepared through recombinant means as fusion proteins.

The at least one "immunogen" which forms part of a complex of the invention is any molecule which it is desirable to use to raise an immune response. Typically,

the at least one "immunogen" will be a molecule which is poorly immunogenic, but immunogenic molecules are not excluded. The at least one "immunogen" includes peptides, oligosaccharides, polypeptides, polysaccharides and specific examples include:
circumsporozoite surface protein of Plasmodium falciparum (CSP); the synthetic immunogen NH_2 Cys (Asn Pro Asn Ala)$_4$ (SEQUENCE ID No. 8) derived from CSP; all or part of luteinizing hormone or somatostatin; and immunogenic proteins which are all or part of: the S protein of hepatitis B virus; the AIDS virus; influenza virus; or foot and mouth disease virus; inhibin and FSH.

With regard to the construction of fusion proteins the invention provides a hybrid first polynucleotide molecule which consists of: a polynucleotide sequence which acts as a coding sequence for at least one T-cell epitope of the invention fused to a polynucleotide sequence coding for the amino acid sequence of at least one immunogen.

The hybrid polynucleotide molecule may comprise sequences encoding: at least one isolated T-cell epitope of the invention fused to at least one immunogen; at least one T-cell epitope of the invention inserted within an immunogen; or all or part of the TraT molecule with the at least one immunogen inserted adjacent a T-cell epitope of the invention.

It is recognised that having provided a sequence encoding a particular fusion protein of interest that it would be within the capabilities of a skilled addressee to alter that sequence so that it still encodes a fusion protein having the activity of the parent fusion. One reason such altered fusions can be prepared is because of the degeneracy of the genetic code. Further a skilled addressee would recognise that it is possible to substitute codons for amino acids with similar characteristics at places within a protein without affecting the activity of the molecule as the parent molecule. Further, having identified a desirable fusion

or complex it could be modified by inclusion of multimers of the T-cell epitope, and/or the immunogen and/or the introduction of additional T-cell epitopes of the invention. Such altered molecules are also within the scope of this invention.

Preferred hybrid polynucleotide sequences are DNA sequences.

More preferably the sequences of the invention coding for at least one T-cell epitope of the invention are linked to a DNA sequence coding for the amino acid sequence of the at least one immunogen such that the resulting TraT fusion protein is exported to and exposed on the host cell surface.

The invention also provides a fused gene comprising a hybrid DNA sequence of the invention fused to a portable promoter. A preferred promoter according to the invention, is the P_L promoter of the bacteriophage lambda.

Further, the invention provides a recombinant DNA molecule which comprises a DNA sequence of the invention and vector DNA. Typically the vector is plasmid, bacteriophage, viral or cosmid DNA.

A preferred recombinant DNA molecule of the invention includes an expression control sequence operatively linked to the DNA sequence of the invention.

Within the scope of the invention is a process for the manufacture of a recombinant DNA molecule which process comprises the step of: introducing into vector DNA, a DNA sequence of the invention.

The process preferably also includes the step of introducing an expression control sequence into the vector.

The invention also provides a transformant host with the genetic information for the biosynthesis of a complex comprising at least one immunogen and at least one T-cell epitope of the invention such that the resulting fused peptide is exposed on the host cell surface.

However, transformant hosts which only express the fusion intracellularly may also be used with the fusion

being purified from the cells in accordance with standard purification procedures.

Suitable hosts include prokaryotic and eukaryotic cells, including: bacteria, for example E. coli, Pseudomonas species, Salmonella species and Bacillus species; yeasts and other fungi, for example Saccharomyces cerevisiae and Aspergillus species; insect cells, for example cell lines derived from Spodoptera frugiperda and Bombyx mori; and mammalian cells for example Chinese Hamster ovary cells and other cell lines.

Also included within the scope of the invention is a process for transforming a host, which process comprises the step of: introducing into a host a recombinant DNA molecule according to the invention.

The invention further provides an expression product of a transformant host of the invention, comprising a complex of the invention.

Brief Description of the Drawings

Figure 1 shows the T-cell response to T1-T7 (SEQUENCE ID Nos 9-15), PHA and TraT (SEQUENCE ID No. 16) in immunized animals.

Figure 2 shows the presentation of T1-T7 (SEQUENCE ID Nos 9-15), PHA and TraT (SEQUENCE ID No. 16) by fixed and control macrophages.

Figure 3 shows T-cell responses to carrier and peptide in monkeys immunized with Pre S2-TraT or PreS2-DT in various formulations.

Figure 4 shows the structure of p TraT (c), a TraT expression vector. P_L = Leftward promoter of Lambda; TT = transcription terminator; Amp^r = Ampicillin resistance gene; Region 1302-3597 approximately equals region 2066 (old PvuII site) to 4367 (old EcoRI site) of pBR322; Diagram not to scale.

Figure 5 shows the coding sequence of TraT and the location of TraT (T1-T7). (SEQUENCE ID Nos 1, 2, 23, 4 ,5 24 and 25).

Best Mode of Carrying Out the Invention

The recombinant DNA techniques, techniques of chemical synthesis, formulation and vaccination used in

accordance with this invention are standard techniques known to those skilled in the appropriate arts. For formulating the vaccines of the invention an effective amount of a complex of the invention is formulated with a pharmaceutically acceptable carrier, diluent, excipient and/or adjuvant to provide a vaccine for administration to a host requiring immunisation with the immunogen of interest.

Solid dosage forms suitable for oral administration may include capsules, tablets, pills, powders, and granules. In such solid dosage forms, at least one complex may be admixed with at least one inert diluent such as sucrose, lactose or starch. Such dosage forms may also comprise, as is normal practice, additional substances other than inert diluents, e.g., lubricating agents such as magnesium stearate. In the case of capsules, tablets, and pills, the dosage forms may also comprise buffering agents. Tablets and pills can additionally be prepared with enteric coatings.

Liquid dosage forms for oral administration may be in the form of pharmaceutically acceptable emulsions, syrups, solutions, suspensions, and elixirs containing inert diluents commonly used in the art such as water. Such compositions may also comprise wetting agents, emulsifying and suspending agents, and sweetening, flavouring, and perfuming agents including sugars such as sucrose, sorbitol, fructose etc, glycols such as polyethylene glycol, propylene glycol etc, oils such as sesame oil, olive oil, soybean oil etc., antiseptics such as alkylparahydroxybenzoate etc, and flavours such as strawberry flavour, peppermint etc.

Suitable excipients, carriers and/or diluents for use in preparation of injectable forms may also be used in preparing injectable vaccines.

Other alternatives would include nasal sprays and other mucosal routes of administration such as suppositories.

The term "pharmaceutically acceptable adjuvant" can mean either the standard compositions which are suitable

for human administration or the typical adjuvants employed in animal vaccinations.

At present alum is the only registered adjuvant for human use however, experimental work is being conducted on other adjuvants for human use and it is anticipated that these other adjuvants would be suitable for use in preparing compositions for human vaccination in accordance with this invention.

Suitable adjuvants for the vaccination of animals include but are not limited to saponin, oil emulsions such as Freund's complete or incomplete adjuvant (not suitable for livestock use), Marcol 52: Montanide 888 (Marcol is a Trademark of Esso. Montanide is a Trademark of SEPPIC, Paris), squalane or squalene, Adjuvant 65 (containing peanut oil, mannide monooleate and aluminium monostearate), mineral gels such as aluminium hydroxide, aluminium phosphate, calcium phosphate and alum, surfactants such as hexadecylamine, octadecylamine, lysolecithin, dimethyldioctadecylammonium bromide, N,N-dioctadecyl-N',N'-bis(2-hydroxyethyl) propanediamine, methoxyhexadecylglycerol and pluronic polyols, polyanions such as pyran, dextran sulfate, polyacrylic acid and carbopol, peptides and amino acids such as muramyl dipeptide, dimethylglycine, tuftsin and trehalose dimycolate. The complexes of the present invention can also be administered following incorporation into liposomes or other micro-carriers, or after conjugation to polysaccharides, proteins or polymers or in combination with Quil-A to form immunostimulating complexes.

It is recognised that a number of factors will affect the determination of an appropriate dosage for a particular host. Such factors include the age, weight, sex, general health and concurrent disease status of the host. The determination of the appropriate dose level for the particular host is performed by standard pharmaceutical techniques.

The strength of the peptide sequences derived from TraT was evidenced by the demonstration that in squirrel monkeys conjugates of TraT and a peptide HepB-preS2 133-152: SEQUENCE ID No. 17 (where PreS2 represents amino acids 120-145 of the preS2 region of Hepatitis B surface antigen) induced a much stronger T-cell response than conjugates of Diphtheria toxoid (DT) and preS2. DT is an effective carrier protein, with a number of T-cell epitopes, which has been approved for use as a carrier in human vaccines.

EXAMPLE 1:

The synthesis of peptides derived from TraT.

The seven peptides, T1 to T7 (SEQUENCE ID Nos 1-7), were synthesized on an Applied Biosystems No. 430A peptide synthesizer with N-terminal pyroGlu and C-terminal Cys-NH_2. The peptides were purified by chromatography on G-25 Sephadex (Pharmacia) in 10% Acetic Acid, followed by Reverse Phase HPLC on a VYDAC C-18 column using a linear gradient of 5-60% acetonitrile in 0.1% TFA. The sequences of the peptides synthesised are as follows:

T1: PyroGluGlyAlaMetSerThrAlaIleLysLysArgAsnLeuGluValLysThr GlnMetSerGluThrIleTrpLeuGluCys-NH_2 (SEQUENCE ID No. 9)

T2: PyroGluGlyLeuGlnGlyLysIleAlaAspAlaValLysAlaLysGlyCys-NH_2 (SEQUENCE ID No. 10)

T3: PyroGluSerGlnTrpLeuAsnArgGlyTyrGluGlyAlaAlaValGlyAlaAla LeuGlyAlaGlyIleThrGlyCys-NH_2 (SEQUENCE ID No. 11)

T4: PyroGluGlyLeuAlaAlaGlyLeuValGlyMetAlaAlaAspAlaMetValGlu AspValAsnCys-NH_2 (SEQUENCE ID No. 12)

T5: PyroGluAspValGlnIleAlaGluArgThrLysAlaThrValThrThrAspAsn ValAlaAlaLeuArgGlnCys-NH_2 (SEQUENCE ID No. 13)

T6: PyroGluSerThrGluThrGlyAsnGlnHisHisTyrGlnThrArgValValSer AsnAlaAsnLysCys-NH_2 (SEQUENCE ID No. 14)

T7: PyroGluLysValAsnLeuLysThrGluGluAlaLysProValLeuGluAspGln LeuAlaLysCys-NH_2 (SEQUENCE ID No. 15)

Purification of TraT

E. coli cells (Strain BTA 1349 containing the plasmid pBTA439, a derivative of plasmid pBR329 into which has been inserted a 6.0 kb EcoR1 fragment of the R100 plasmid which contains the DNA sequence coding for TraT, expressed from the lambda leftward promoter P_L), were grown in a fermenter at 30°C and induced at 42°C for 2 hours. Following induction, the cells were concentrated and washed with distilled water in an Amicon DC10LA concentrator (0.1µm hollow fibre cartridge). Cells were removed from the concentrator and the integral membrane proteins extracted from the cells by the addition of a solution containing 0.2M Na Acetate buffer pH 2.5, 2% cetrimide (Sigma) in 20% ethanol plus 0.2 M $CaCl_2$ (final concentration). The extraction was allowed to proceed overnight at room temperature (RT) after which the bacteria were pelleted by centrifugation (17,000 x g, 20 min.).

TraT was precipitated from the supernatant by the addition of ethanol to 50% followed by centrifugation (4000 x g. 10 min). It was then resuspended in 1% Zwittergent, 20 mM Na Acetate buffer, pH 6.5, 20 mM EDTA and further purified by chromatography on DEAE-Sepharose (Pharmacia) in 20mM Na Acetate buffer pH 6.5, containing 0.1% Zwittergent (Calbiochem) and 20 mM EDTA. Proteins were eluted using a linear gradient of 0 to 1 M NaCl in the loading buffer. Fractions containing the integral membrane proteins were pooled, precipitated with ethanol

and resuspended in 10% SDS and further purified by size exclusion chromatography on S-300 Sephacryl (Pharmacia) in 10 mM Tris. HCl pH 8.8 containing 2% SDS, 20 mM EDTA. TraT purified by this method travelled as a single band when analyzed by SDS-PAGE with a molecular weight of 28,000, and was found to be free of LPS when subjected to SDS-PAGE and silver stained by the method of Tsai and Frasch (Anal. Biochem. 119: 115, 1982). The TraT protein was found to be contaminated with less than 0.005 ng of LPS/mg of protein when tested in the LAL assay (Webster, J Clin Microbiol. 12: 644, 1980).

Immunization of animals and the assessment of T-cell proliferation.

Animals were immunized intramuscularly with 50 µg (mice), 200 µg (dogs and monkeys) or 500 µg (cattle) of TraT in saline and boosted 14 to 28 days later with a similar inoculum. Fourteen days after the last injection, peripheral blood lymphocytes (dogs, monkeys and cattle) or lymph node cells (mice) were used as a source of T lymphocytes which were then stimulated in vitro with various concentrations of the peptides [the responses to 50µg of TraT (SEQUENCE ID No. 16) and 50µg of T1 to T7 (SEQUENCE ID Nos 9-15, respectively) as well as to 2µg PHA are given in Figure 1]. T-lymphocytes were isolated from lymph nodes according to the method of Adorini et al. J. Exp. Med. 168: 2091, 1988; while the method of Chouaib et al. (P. N. A. S., 85: 6875, 1988) was followed for the isolation of T-cells from peripheral blood. The method of Adorini et. al. was followed for the assessment of T-cell proliferation. Results are expressed as Stimulation indices, which are calculated by dividing the c.p.m. in the presence of antigen by the c.p.m. in the absence of antigen. Standard errors of the means of triplicate cultures were less than 10% of the Mean.

Results

As can be seen from Figure 1, significant T-cell responsiveness to 50 µg of T1, T2, T4 and T6 (SEQUENCE ID Nos 9, 10, 12 and 14 respectively) as well as to TraT was seen in all four species, with T2, T4 and T6 (SEQUENCE ID Nos. 10, 12 and 14 respectively) showing particularly strong responses. The high degrees of conservation of the responses to these peptides in a number of species suggests that these peptides may prime for strong antibody responses in a range of phylogenetically diverse species as well as in a range of genetically diverse individuals within a species. T-cell stimulatory peptide sequences that cross several species barriers have not, to our knowledge, been reported in the literature.

Primary and secondary T-cell proliferative responses of human peripheral blood lymphocytes to TraT and to the T-cell epitope peptides

The strong in vitro proliferative responses observed to the T-cell peptides (in particular to T2, T4 and T6: SEQUENCE ID Nos 10, 12 and 14 respectively) in the four animal species studied, suggested that a similar hierarchial pattern of responsiveness would also be seen in humans. T-cell epitope peptides which exhibit a permissive association with major histocompatibility complex (MHC) molecules, and are therefore preferentially recognised by T-cells, would be attractive candidates for the production of subunit vaccines because they would be expected to induce an immune response in the majority of individuals in a outbred human population. It was therefore decided to examine T-cell responses in humans to TraT-derived T-cell epitopes.

Because of the logistic problems posed by immunizing humans with TraT (to our knowledge none of the blood donors had been deliberately immunized with TraT), an alternative approach involving in vitro immunization was performed.

To test the "universality" of the TraT-derived T-cell stimulatory peptides in humans, heparinized blood samples were obtained from twenty randomly selected donors at a Blood Bank. Peripheral blood lymphocytes (PBL), which are an enriched T-cell population, were stimulated in vitro with TraT or with T1 to T7 (SEQUENCE ID Nos 9-15) in primary cultures, and a portion of the PBL was also restimulated with TraT-pulsed mononuclear cells in secondary cultures. The results in Table 1 show that, in a 3-day primary T-cell proliferation assay, PBL of eight from twenty (40%) donors responded (stimulation index $\geq$ 3) to at least three (T2, T4, T6: SEQUENCES ID Nos 10, 12 and 14 respectively) of the T-cell peptides as well as TraT (SEQUENCE ID No. 16). However, after a secondary in vitro immunization with TraT-pulsed PBL, responsiveness was observed in the cultures derived from all twenty donors (Table 2) and in addition, a significant boosting effect was seen in cell cultures which responded to primary stimulation. The important implication of this work is that T-cell stimulatory peptides such as T2, T4, T6 (SEQUENCE ID Nos 10, 12 and 14) and possibly T1 (SEQUENCE ID No. 9) could be employed as carriers in subunit vaccines and thereby overcome the unresponsiveness observed in humans as a result of MHC restriction.

Table 1

Primary T-cell proliferative responses of human peripheral blood lymphocytes to TraT and the T-cell stimulatory peptides

	In vitro Stimulants								
DONOR	T1	T2	T3	T4	T5	T6	T7	TraT	PHA
R.E.	1.0	1.2	0.7	1.1	0.7	12.8	1.2	10.3	86
A.L.	15.8	22.9	1.2	15.8	2.8	31.0	0.9	42.5	56.2
N.M.	6.4	8.0	1.8	10.7	3.0	10.3	1.7	7.8	191
S.S.	0.8	0.8	0.7	0.8	3.8	0.6	0.6	3.9	133
C.O.	1.0	0.7	1.1	0.7	1.0	1.0	1.0	1.1	105
B.G.	0.9	0.9	0.8	0.8	0.7	0.8	0.8	1.0	90.6
A.W.	3.9	6.9	2.8	6.8	2.7	8.8	0.9	9.0	84.3
B.F.	0.7	1.0	1.1	1.2	1.0	4.7	1.1	4.6	141.0
G.F.	1.0	2.0	1.2	1.4	1.5	82.8	1.9	70.8	183.0
S.S.	29.1	51.1	15.7	48.3	23.1	73.0	0.8	68.2	84.9
D.H.	28.4	43.8	8.4	52.7	25.2	65.4	0.9	70.6	97.8
C.B.	1.1	1.1	1.3	2.1	2.5	22.2	1.1	49.2	139
G.L.	1.0	0.8	1.4	1.0	1.0	1.8	1.1	1.1	357
Z.L.	0.9	0.8	0.6	1.1	1.5	0.8	0.8	0.6	217
D.W.	69.7	10.8	30.4	100.0	39.0	184.5	1.9	155.0	223
F.W.	0.8	0.7	0.7	2.0	2.0	34.6	2.8	60.5	117
K.M.	0.8	31.0	17.0	37.5	18.0	47.0	0.8	41.4	51.3
S.M.	17.3	26.7	1.0	42.7	29.5	53.4	0.8	51.5	71.0
R.T.	2.0	0.9	1.0	0.9	0.8	1.0	0.9	1.3	57.2
J.L.	1.0	0.5	0.5	0.7	0.7	0.5	0.6	0.7	57.2

Peripheral blood lymphocytes (PBL) were separated from heparinized blood by Ficoll-Paque (Pharmacia) gradient centrifugation. Briefly, 10 ml of blood were layered on 6 ml of Ficoll Paque and an enriched T-cell population was separated by centrifugation at 400g for 40 min. PBL (10^5 in 0.2ml RPMI medium containing 10% human AB serum) were cultured in flat-bottom plates with 50µg of TraT (SEQUENCE ID No. 16) or one of the T-cell stimulatory peptides (T1 to T7; SEQUENCE ID Nos 9-15) or with 2µg PHA

for 3 days at 37°C. Sixteen hours before harvesting, cells were labelled with 0.5µCi of tritiated thymidine, harvested and counted in a liquid scintillation counter. Results are expressed as Stimulation Indices which are calculated by dividing the counts per minute (c.p.m.) in the presence of antigen by c.p.m. in the absence of antigen.

Table 2

Secondary T-cell proliferative responses of human peripheral blood lymphocytes to TraT and the T-cells stimulatory peptides

	In vitro Stimulants								
DONOR	T1	T2	T3	T4	T5	T6	T7	TraT	PHA
R.E.	6.1	10.6	4.1	12.3	3.8	17.0	1.6	15.9	227.0
A.L.	11.8	38.0	1.8	45.0	3.6	59.0	1.8	66.0	218.0
N.M.	7.8	24.2	3.8	36.0	4.5	55.2	3.3	72.0	274.0
S.S.	1.0	11.8	5.7	12.5	0.8	14.7	1.3	16.8	379.3
C.O.	9.2	15.8	5.9	18.3	5.3	23.2	0.6	49.2	110.5
B.G.	35.2	46.7	18.1	50.7	27.7	72.8	1.0	78.3	357.0
A.W.	2.6	25.0	5.3	42.3	6.2	55.9	2.4	66.2	317.0
B.F.	49.8	110.0	32.0	161.0	73.0	227.0	2.2	235.0	113.0
G.F.	1.3	32.0	20.0	56.0	24.5	71.5	1.5	89.4	160.0
S.S.	23.0	51.5	14.2	69.4	40.0	110.0	8.0	133.0	309.0
D.H.	32.3	49.0	7.7	86.0	20.8	133.0	2.5	166.6	335.0
C.B.	6.7	13.1	4.3	18.4	1.2	19.2	4.7	63.5	304.0
G.L.	2.6	41.5	1.0	28.3	2.3	22.0	5.4	17.9	206.0
Z.L.	0.8	119.0	90.0	135.0	102.0	150.0	0.5	125.0	104.3
D.W.	56.0	150.0	28.0	185.0	26.5	216.0	2.8	236.0	116.5
F.W.	3.2	27.5	1.9	43.0	3.8	72.0	3.9	186.0	180.2
K.M.	32.0	62.5	8.6	62.6	12.5	93.0	2.8	120.5	175.3
S.M.	8.2	32.5	2.9	66.5	15.4	92.5	2.2	146.0	218.0
R.T.	1.2	226.0	74.6	270.0	45.7	255.0	1.0	289.0	195.0
J.L.	1.0	251.0	53.0	205.0	1.2	202.0	1.8	289.0	226.0

PBL (6 to 7 x 10^6) were pulsed with 50µg TraT (SEQUENCE ID No. 16) for 30 min at 37°C and then washed three times with RPMI medium containing 10% human AB serum. The antigen-pulsed cells were set up in 3ml culture medium in 30-ml culture flasks (Costar) and then incubated upright for 8 days at 37°C. A portion of the PBL was set aside and frozen in 10% dimethyl sulphoxide and subsequently used to stimulate the primary cultures. At the end of the primary incubation, the cells were centrifuged at 150g for 10 min and then stimulated with 2 x 10^6 TraT-pulsed frozen and thawed PBL and the restimulated cultures incubated in culture flasks for a further 3 days at 37°C. Viable cells (3 to 4 x 10^6) recovered at the end of the secondary culture were washed twice, resuspended at concentration of 10^6 cells/ml of culture medium and 10% human AB serum. The restimulated PBL (10^5 in 0.2ml Culture Medium) were finally cultured in flat-bottom plates with TraT (SEQUENCE ID No. 16), T1 to T7 (SEQUENCE ID Nos 9 to 15) or PHA for 3 days as previously described (see legend to Table 1).

T-cell stimulatory peptides from TraT are stronger than those from Diphtheria toxoid (DT)

The in vitro activities of TraT-derived peptides (T1 to T6: SEQUENCE ID Nos 9-14) were compared with those of four peptides reported by others (D1 and D2: SEQUENCE ID Nos 19 and 20; Bixler et al. PCT/US89/00388) or predicted (D3 and D4: SEQUENCE ID Nos 21 and 22) to have strong T-cell stimulatory activity prepared with N and/or C-terminal modification. DT is widely used as a carrier molecule for providing T-cell help for immunogens conjugated to it. For ethical reasons it was not possible to immunise humans with TraT (SEQUENCE ID No. 16). Therefore normal blood donors whose lymphocytes responded to both DT and TraT in vitro were chosen; about 60% of randomly selected blood donors respond to TraT in vitro (see Table 1). The data in the Table 3 below show that in four out of five of those individuals, the responses to the TraT molecule were at least as high as those to DT. Furthermore, the proliferative responses induced by T4 (SEQUENCE ID No. 12) and T6 (SEQUENCE ID NO. 14) in primary cultures were 2- to 3-fold higher than by any of the DT-derived peptides (D1 to D4: SEQUENCE ID Nos 19 to 22). Note that the responses to T6 (SEQUENCE ID No. 14) are almost as strong as those to the TraT molecule itself, suggesting that T6 has an extremely high binding affinity for the MHC. In contrast, the responses to D1 and D4 (SEQUENCE ID Nos 19 and 22) are much lower than to the native DT molecule.

These results show that at least two of the TraT-derived peptides have stronger T-cell stimulatory activity than any of the four selected DT-derived sequences and hence the data indicate the superior utility of these molecules in human vaccine formulations.

Table 3

T-cell stimulatory activity of peptides from TraT and Diphtheria toxoid (DT)

Stimulant (in vitro)	Human Donors 1	2	3	4	5
T1	2.4*	1.8	2.3	6.2	20.4
T2	5.6	6.6	8.2	33.2	32.0
T3	1.2	2.0	1.8	13.0	12.7
T4	12.8	14.2	16.6	49.3	49.5
T5	3.4	2.8	3.2	7.7	26.2
T6	16.9	18.9	22.4	56.6	45.2
T7	2.8	2.1	3.8	14.5	18.6
TraT	20.6	24.2	28.7	64.5	48.5
DT	19.4	40.1	18.8	62.6	34.7
D1	4.2	3.8	5.9	23.1	20.7
D2	1.1	0.9	1.9	17.3	13.9
D3	5.8	4.2	6.6	20.8	18.5
D4	4.7	5.7	7.3	26.0	23.2
PHA	186.0	192.0	238.0	69.3	57.3

*Stimulation Index

For details of procedures for assessing T-cell proliferation see the legend to Table 1. T-cells were cultured with 50µg of TraT, T1 to T7, DT and D1 to D4 or with 2µg PHA for 3 days at 37°C.

EXAMPLE 2

The Immunogenic Fragment(s) Formed as a Result of "Natural" Processing of TraT Appear to Interact with Major Histocompatability Complex (MHC) Class II Antigens at Least as Effectively as the Peptides T1, T2, T4 and T6. (SEQUENCE ID Nos 1, 2, 4 and 6).

Immunization of animals and antigen presentation by macrophages.

Mice (CBA or C57BL/6J) were immunized subcutaneously with 50 µg TraT (SEQUENCE ID No. 16) in saline and 10 days after priming, the animals were injected intraperitoneally with 1 ml Marcol oil to induce a peritoneal exudate (PE). Three days later, the mice were sacrificed, the PE harvested and the macrophages separated as described by Buus and Werdelin (J. Immunol. 136: 452, 1986). Macrophages were fixed with paraformaldehyde, essentially as described by Buus and Werdelin (see above). Briefly, macrophages (5×10^6) were treated with 1% paraformaldehyde in 0.1M PBS for 2 min. and the reaction was stopped by the addition of 0.15M glycine-PBS buffer. The fixed macrophages were washed three times in buffer, suspended in RPMI (10% FCS) and 10^5 cells pulsed with TraT (SEQUENCE ID No. 16) (50µg), PHA (2µg) or with the peptides, T1 to T7 (SEQUENCE ID Nos 9-15) (50µg) for 30 min. at 37°C; unfixed or control macrophages were also pulsed with antigen for 30 min. at 37°C. After three washes to remove excess antigen, 10^5 antigen-pulsed paraformaldehyde-fixed or untreated macrophages were combined with 10^5 TraT-immune T lymphocytes (prepared as described in EXAMPLE 1) and the cells incubated for 72 h at 37°C. Stimulation was determined as described in the previous section.

Results

As shown in Figure 2, fixed macrophages were almost as efficient as untreated macrophages in presenting the four peptides T1, T2, T4 and T6 (SEQUENCE ID Nos 9, 10, 12

and 14) to T lymphocytes, although T6 (SEQUENCE ID No 14) appears to require more processing than the other three peptides. By contrast, fixed macrophages were unable to present the native TraT molecule, presumably because TraT needs to be processed by viable macrophages before it is recognized by T-cells. The data therefore, suggest that the fragments which result from natural processing of TraT, must be very similar to the TraT derived peptides in terms of their interaction with Class II molecules on the surface of the macrophage. If the peptide fragments derived from TraT were vastly different from the naturally processed fragments they would not without further processing interact with macrophages to stimulate T-cells. It is of interest that these Class II molecules appear to remain intact despite the paraformaldehyde treament. These observations further suggest that the four peptides, T1, T2, T4 and T6 (SEQUENCE ID Nos 1, 2, 4 and 6), may indeed play an important role in the generation of antibody responses in vivo.

EXAMPLE 3

In Squirrel Monkeys, PreS2-TraT Conjugates Induce Stronger T-cell Responses than PreS2-Conjugates of Diphtheria Toxoid (DT).

Synthesis of peptide and its conjugation to the Carrier.

A peptide containing part of the highly immunogenic preS2 peptide (amino acids 120-145 of the preS2 region of Hepatitis B) plus some further sequence consisting of amino acids 133-152 viz.

Asp-Pro-Arg-Val-Arg-Gly-Leu-Tyr-Phe-Pro-Ala-Gly-Gly-Ser-Ser-Ser-Gly-Thr-Val-Cys: SEQUENCE ID No. 17) was synthesized on an Applied Biosystems No. 430A peptide synthesizer. The peptide was purified by chromatography on G-25 Sephadex (Pharmacia) in 10% Acetic Acid, followed by Reverse Phase HPLC on a VYDAC C-18 column using a linear gradient of 5-60% acetonitrile in 0.1% TFA.

Diphtheria toxoid (DT); (Commonwealth Serum Laboratories, Melbourne, Australia, 1570 Lf units/ml) was precipitated in 80% ethanol and resuspended in 0.1M Phosphate buffer, pH7.0. It was then activated with a 60-fold molar excess of m-maleimido benzoic acid n-hydroxysuccinimide ester (MBS, Sigma Chemical Co; made up at 10mg/ml in DMF) for 30 min. at 22°C. The activated DT was precipitated with 80% ethanol, resuspended in 0.1M Phosphate buffer, pH7.0 and mixed with a 20-fold molar excess of preS2 peptide for 3 hr. at 22°C. The conjugate was dialysed overnight against PBS.

TraT was precipitated in 50% ethanol, resuspended in 50mM Phosphate buffer, pH 7.0 containing 1% Zwittergent and activated with 10-fold of MBS for 30 min. at 22°C. The activated TraT was mixed with a 14-fold molar excess of preS2 (SEQUENCE ID No. 17) peptide for 3 hr. at 22°C. The conjugate was then dialysed overnight against PBS containing 0.1% Zwittergent. The average number of preS2 groups (based on amino acid analysis) per molecule of protein carrier were 2 (TraT) and 10 (DT) respectively.

Formulations

Alhydrogel: PreS2-TraT or PreS2-DT (2.5 mg in 0.5 ml) was added to 0.5ml of alhydrdogel and made up to 2.5ml with PBS and Zwittergent (0.5%).

Saponin: PreS2-TraT or PreS2-DT (2.5mg in 0.5ml) was added to 2.5mg Saponin and then made up to 2.5ml with PBS.

Zwittergent: TraT- or DT- conjugates (2mg in 0.5ml) were made up to 2ml with PBS and Zwittergent (0.5%).

Liposomes: (A) TraT- or DT- conjugates, following precipitation with 80% ethanol, were resuspended in 1ml of 10% octylglucoside in 10mM Hepes.
(B) 1 ml of chloroform containing phosphatidyl ethanolamine (16mg) and phosphatidylcholine (4mg) were placed in a flask and the chloroform evaporated off under vacuum.
1ml of the octylglucoside solution (A) was added to (B) and the formulation solubilized by sonication, followed by overnight dialysis against PBS.

Squirrel monkeys were immunized intramuscularly on days 0 and 42 with 200µg of each of the conjugates (preS2-TraT or preS2-DT) in the various formulations (zwit=zwittergent; AlOH=Alhydrogel; Sap=Saponin; Lip=Liposomes). Peripheral blood lymphocytes taken at day 56 were used as a source of T-cells which were then stimulated in vitro with various concentrations of TraT, DT or preS2 as described in EXAMPLE 1. Results (Proliferative responses to 50µg of TraT, DT or preS2) are expressed as Stimulation indices. Standard errors of the means of triplicate cultures were less than 10% of the Mean.

Results

The results in Figure 3 show that T-cell proliferative responses to TraT were 2- to 3-fold higher than to Diphtheria toxoid. Furthermore, the anti-PreS2 responses

in PreS2-TraT-immunized monkeys were 3- to 4-fold higher than in PreS2-Diphtheria toxoid-immunized animals. The superior T-cell responses generated in response to TraT suggests that this protein (or one of its T-cell stimulatory sequences) may be a useful component of vaccines especially those against viral and parasitic diseases. There is impressive evidence that for many viral and parasitic infections, effector T-cells are primarily responsible for clearance of the infection.

EXAMPLE 4

Peptide Sequences (T2, T4, T6: SEQUENCE ID Nos 2, 4 and 6) Derived from TraT Prime for Strong Antibody Responses to a Peptide Attached to Them.

After we had identified and documented the existence of strong T-cell stimulatory peptide sequences within TraT, it was necessary to determine whether the delineated regions of TraT could function as effective carrier molecules. The peptide gp120 (amino acids 254-274 of the conserved domain of the gp120 region of HIV1) was used to provide an antigenic determinant. The ability of T-cell stimulatory sequences to deliver T-cell help and therefore prime for antibody responses to peptides attached to them, is an important feature of T-cell epitope peptides. Accordingly, mice were immunized with glutaraldehyde conjugates of each of the seven peptides T1 to T7 (SEQUENCE ID Nos 9-15) and the gp 120 peptide, emulsified in Montanide/Marcol (9:1) adjuvant, and boosted 21 days after the primary immunization. The antibody responses elicited in these animals are depicted in Table 4. These results show that the peptides (T2, T4 and T6: SEQUENCE ID Nos 10, 12 and 14) that elicited strong T-cell responses also primed for the highest antibody responses to the peptide gp120 demonstrating their utility as carriers. Because these peptides have strong T-cell stimulatory activity, poor to negligible antibody levels were seen in response to the strong peptides (T2, T4 and T6: SEQUENCE ID Nos 10, 12 and 14) themselves.

Preparation of Glutaraldehyde conjugates of gp120 peptide and the T-cell epitope peptides.

The two-step glutaraldehyde procedure of Avrameus et al. (Scand. J. Immunol. 8: 7, 1978) was followed. Briefly, the gp120 peptide (1mg/ml) in 0.1M PBS pH 6.8 was reacted with 0.2% glutaraldehyde for 2 hr. at 22°C. Following overnight dialysis against 0.1M carbonate/bicarbonate buffer pH 9.5, the glutaraldehyde activated gp 120 was added to the various peptides (T1 to T7: SEQUENCE ID Nos 9-15) at a molar rate of 1:1 and reacted for 24 hr at 22°C. The conjugates were suspended in 1ml of PBS and emulsified in Montanide/Marcol (9:1).

Groups of five female C57BL/6J mice (20-25g) were immunized subcutaneously on days 0 and 21 with 100µg of glutaraldehyde conjugates of each of the peptides (T1 to T7: SEQUENCE ID Nos 9-15) and the gp 120 peptide, emulsified in Montanide/Marcol (9:1) or with the gp120 peptide in saline. Animals were bled at 14 days after the second injection and anti-carrier (T1 to T7: SEQUENCE ID NOs 9-15) and anti-peptide (gp120) responses were estimated by a standard ELISA using plates coated with the T1 to T7 (SEQUENCE ID Nos 9-15) peptides or with gp120.

Results

The results in Table 4 show that the T-cell stimulatory peptides T2, T4, T6 (SEQUENCE ID Nos 10, 12 and 14) and possibly T1 (SEQUENCE ID No. 9) primed for the highest antibody responses to the peptide (gp 120) attached to them. As anticipated, weak to negligible antibody titres were seen in response to these peptides (T1, T2, T4 and T6: SEQUENCE ID Nos 9, 10, 12 and 14). Because they are T-cell epitopes they are unlikely to stimulate B cells well. By contrast, virtually no response was seen in animals immunized with gp120 in saline. Therefore these T-cell stimulatory peptides will be useful for priming antibody responses to peptide antigens. Such antigens of commercial utility may include but are not limited to luteinising hormone, somatostatin,

inhibin, FSH,foot and mouth disease peptide, Hepatitis B pre S2 peptide, malaria peptides, Herpes or influenza peptides.

TABLE 4

Anti-Carrier and Anti-Peptide responses in mice immunized with gp 120 -T-cell stimulatory peptide conjugates.

ANTIBODY RESPONSE

Immunization Groups	Anti-Carrier	Anti-gp-120 peptide
Saline	1	1
gp 120-T1	2	838
gp 120-T2	1	2,612
gp 120-T3	1,234	52
gp 120-T4	1	3,110
gp 120-T5	2	158
gp 120-T6	3	3,431
gp 120-T7	400	13
gp 120	1	13

Antibody titres are expressed as the arithmetic mean of the reciprocal of the antiserum dilution which gave an ELISA reading of 0.5 after 45 min. at 25°C.

The strong T-cell stimulation observed with these peptides that prime for B-cell responses to the attached immunogen could also be achieved by the incorporation of the T-cell epitope sequences into fusion proteins specifically designed for the presentation of peptide antigens.

Immunogenic fusion proteins comprising the T-cell epitopes and protein or peptide antigens can be produced from a recombinant gene encoding the fusion protein when expressed in an appropriate host-vector system. These chimaeric proteins may take various forms. The antigen

may be located adjacent to the T-cell epitope such as T2 (SEQUENCE ID No 2) or T6-(SEQUENCE ID No. 24) with TraT essentially intact (for example, luteinising hormone releasing hormone [LHRH]/ TraT fusions); the T-cell epitopes alone may be inserted within the protein antigen. For example T2 (SEQUENCE ID No. 2) or T6 (SEQUENCE ID No. 6 or 24) may be inserted into the tick antigen BM86 (described as WGL^+ in PCT/AU87/00401); or parts of TraT bearing T2 (SEQUENCE ID No. 2) and/or T6 (SEQUENCE ID No. 24) may be located close to antigenic portions of a protein (for example, T2,T6/TraT and luteinising hormone).

A suitable source of DNA encoding the T-cell epitopes of the invention is ATCC 67331.

EXAMPLE 5

Improvement of vaccine efficacy by the use of strong universal T-cell epitopes.

One of the major drawbacks to the development of effective vaccines to diseases such as AIDS, has been the presence in otherwise immunogenic molecules, such as gp120 (an immunodominant external envelope protein of HIV) of "suppressor regions" which interfere with the development of effective immune responses to these proteins. In order to elicit protective immune responses to these proteins it is proposed to remove these sequences and to replace them with more immunogenic sequences.

T-cell epitope sequences derived from TraT possess unexpectedly high immuno-stimulatory properties in a range of phylogenetically diverse species. These diverse T-cell epitope peptides which manifest a permissive association with major histocompatibility complex (MHC) molecules, and are therefore preferentially recognized by T-cells, would be expected to elicit strong T-cell immunity in the majority of individuals in an outbred population.

Two suppressor regions, corresponding to amino acid sequences 735-752 and 846-860 of the transmembrane glycoprotein of HIV, have been shown to exert a marked inhibition of the human blastogenic responses to mitogens and alloantigens (Chanh, T.C., Kennedy, R.C. and Kanda, K. Cell Immunol. 111: 77-86. 1988).

Using recombinant DNA technology, the "suppressor regions" in a number of prospective vaccine proteins including gp 120 are removed and replaced with immunostimulatory peptides derived from TraT. This approach results in vaccines which elicit strong protective immunity in hosts from a broad spectrum of MHC backgrounds. In the first instance the removal of suppressor regions will improve the immunogenicity of the molecule and the replacement of suppressor regions with immunostimulatory regions will further increase the immunogenicity of the modified molecule. The replacement of the suppressor region(s) with a strongly T-cell stimulatory region such as T6, will increase the immunogenicity of the modified recombinant molecule. This molecule would substitute for the native gp120 molecule where this modified molecule is used as a basis of a vaccine e.g. a sub-unit vaccine or as part of inactivated viral particles.

For example, the suppressor region of HIV corresponding to the amino acid sequence (735-752):

Tyr-Asp-Arg-Pro-Glu-Gly-Ile-Glu-Glu-Glu-Gly-Gly-
(735)

Glu-Arg-Asp-Arg-Asp-Arg-Ser-Gly-Cys (SEQUENCE ID No. 18)
(752)

is replaced by the-

TraT-derived T6 peptide:

Ser-Thr-Glu-Thr-Gly-Asn-Gln-His-His-Tyr-Gln-Thr-Arg-Val-Val-

Ser-Asn-Ala-Asn-Lys (SEQUENCE ID No. 6)

Industrial Application

The current invention is of value in the preparation of vaccines for use in animals and humans. The use of T-cell epitope peptides as carrier molecules will enhance antibody production as well as stimulate cell-mediated immunity while avoiding many of the disadvantages of using larger protein carrier molecules.

Deposition of Strains

BTA 1349 was deposited in accordance with the provisions of the Budapest Treaty with the American Type Culture Collection of 12301 Parklawn Drive, Rockville MD 20852 USA on 2 March 1987 under accession number ATCC 67331.

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SEQUENCE LISTING

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(C) CLASSIFICATION:

(VII) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PK2361
(B) FILING DATE: 18 September 1990

(2) INFORMATION FOR SEQ: ID NO: 1 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(A) DESCRIPTION: A sequence tested for T-cell epitope activity from the E. coli protein TraT

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1

Gly Ala Met Ser Thr Ala Ile Lys Lys Arg
5 10
Asn Leu Glu Val Lys Thr Gln Met Ser Glu
15 20
Thr Ile Trp Leu Glu
25

(2) INFORMATION FOR SEQ: ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(A) DESCRIPTION: A sequence tested for T-cell epitope activity from the TraT protein of E. coli

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION : SEQ ID NO. 2

Gly Leu Gln Gly Lys Ile Ala Asp Ala Val Lys Ala Lys Gly

5 10

(2) INFORMATION FOR SEQ: ID NO: 3 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 Amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Sequence tested for T-cell epitope activity derived from the TraT protein of E. coli with N-terminal modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ser Gln Trp Leu Asn Arg Gly Tyr Glu Gly Ala Ala Val Gly Ala
5 10 15

Ala Leu Gly Ala Gly Ile Thr Gly
20

(2) INFORMATION FOR SEQ: ID NO: 4 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Sequence tested for T-cell epitope activity from the TraT protein of E. coli

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Gly Leu Ala Ala Gly Leu Val Gly Met Ala Ala Asp Ala Met Val
5 10 15

Glu Asp Val Asn

(2) INFORMATION FOR SEQ: ID NO: 5 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Sequence tested for T-cell epitope activity from the TraT protein of E. coli

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Val Gln Ile Ala Glu Arg Thr Lys Ala Thr Val Thr Thr Asp
5 10 15

Asn Val Ala Ala Leu Arg Gln
20

(2) INFORMATION FOR SEQ: ID NO: 6 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Sequence tested for T-cell epitope activity derived from the TraT protein of E. coli with modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ser Thr Glu Thr Gly Asn Gln His His Tyr Gln Thr Arg Val Val
5 10 15

Ser Asn Ala Asn Lys
20

(2) INFORMATION FOR SEQ: ID NO: 7 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Sequence tested for T-cell epitope activity derived from the TraT protein of E. coli with modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Val Asn Leu Lys Thr Glu Glu Ala Lys Pro Val Leu Glu Asp
5 10 15

Gln Leu Ala Lys

(2) INFORMATION FOR SEQ: ID NO: 8 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Synthetic immunogen derived from circumsporozoite surface protein of Plasmodium falciparum

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: N/A

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Cys Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro

5 10 15

Asn Ala

(2) INFORMATION FOR SEQ: ID NO: 9 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of Sequence ID No. 1 with added N-terminal and C-terminal residues

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = pyroglutamic acid
At position 27, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Gly Ala Met Ser Thr Ala Ile Lys Lys Arg Asn Leu Glu Val
5 10 15

Lys Thr Gln Met Ser Glu Thr Ile Trp Leu Glu Xaa
20 25

(2) INFORMATION FOR SEQ: ID NO: 10 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 2 with added N-terminal and C-terminal residues

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = pyroglutamic acid
At position 16, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Gly Leu Gln Gly Lys Ile Ala Asp Ala Val Lys Ala Lys Gly
5 10 15

Xaa

(2) INFORMATION FOR SEQ: ID NO: 11 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 3 with added N-terminal and C-terminal residues

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = pyroglutamic acid
At position 25, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ser Gln Trp Leu Asn Arg Gly Tyr Glu Gly Ala Ala Val Gly
5 10 15

Ala Ala Leu Gly Ala Gly Ile Thr Gly Xaa
20 25

(2) INFORMATION FOR SEQ: ID NO: 12 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 4 with added N-terminal and C-terminal residues

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURES: At position 1, Xaa = pyroglutamic acid
At position 21, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Gly Leu Ala Ala Gly Leu Val Gly Met Ala Ala Asp Ala Met
5 10 15

Val Glu Asp Val Asn Xaa
20

(2) INFORMATION FOR SEQ: ID NO: 13 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 5 with N-terminal and C-terminal residues added

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURES: At position 1, Xaa = pyroglutamic acid
At position 24, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Asp Val Gln Ile Ala Glu Arg Thr Lys Ala Thr Val Thr Thr
5 10 15

Asp Asn Val Ala Ala Leu Arg Gln Xaa
20

(2) INFORMATION FOR SEQ: ID NO: 14 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 6 with N-terminal and C-terminal residues added

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = pyroglutamic acid
At position 22, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ser Thr Glu Thr Gly Asn Gln His His Tyr Gln Thr Arg Val
5 10 15

Val Ser Asn Ala Asn Lys Xaa
20

(2) INFORMATION FOR SEQ: ID NO: 15 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Modification of sequence ID No. 7 with added N-terminal and C-terminal residues

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM:
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = pyroglutamic acid
At position 21, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Lys Val Asn Leu Lys Thr Glu Glu Ala Lys Pro Val Leu Glu
5 10 15

Asp Gln Leu Ala Lys Xaa
20

(2) INFORMATION FOR SEQ: ID NO: 16 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double stranded
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
(A) DESCRIPTION: Codes for the TraT protein of E. coli

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: N/A

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E. coli
(B) STRAIN: a strain carrying plasmid R100
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349 (ATCC 67331)

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
AAA ATG AAA AAA TTG ATG ATG GTT GCA CTG GTC AGT TCC ACT CTG    45
Lys Met Lys Lys Leu Met Met Val Ala Leu Val Ser Ser Thr Leu
                  5                  10                  15
GCC CTT TCA GGG TGT GGT GCG ATG AGC ACA GCA ATC AAG AAG CGT    90
Ala Leu Ser Gly Cys Gly Ala Met Ser Thr Ala Ile Lys Lys Arg
                 20                  25                  30
AAC CTT GAG GTG AAG ACT CAG ATG AGT GAG ACC ATC TGG CTT GAA   135
Asn Leu Glu Val Lys Thr Gln Met Ser Glu Thr Ile Trp Leu Glu
                 35                  40                  45
CCC GCC AGC GAA CGC ACG GTA TTT CTG CAG ATC AAA AAC ACG TCT   180
Pro Ala Ser Glu Arg Thr Val Phe Leu Gln Ile Lys Asn Thr Ser
                 50                  55                  60
GAT AAA GAC ATG AGT GGG CTG CAG GGC AAA ATT GCT GAT GCT GTG   225
Asp Lys Asp Met Ser Gly Leu Gln Gly Lys Ile Ala Asp Ala Val
                 65                  70                  75
AAA GCA AAA GGA TAT CAG GTG GTG ACT TCT CCG GAT AAA GCC TAC   270
Lys Ala Lys Gly Tyr Gln Val Val Thr Ser Pro Asp Lys Ala Tyr
                 80                  85                  90
TAC TGG ATT CAG GCG AAT GTG CTG AAG GCC GAT AAG ATG GAT CTG   315
Tyr Trp Ile Gln Ala Asn Val Leu Lys Ala Asp Lys Met Asp Leu
                 95                 100                 105
CGG GAG TCT CAG GGA TGG CTG AAC CGT GGT TAT GAA GGC GCA GCA   360
Arg Glu Ser Gln Gly Trp Leu Asn Arg Gly Tyr Glu Gly Ala Ala
                110                 115                 120
GTT GGT GCA GCG TTA GGT GCC GGT ATT ACC GGC TAT AAC TCA AAT   405
Val Gly Ala Ala Leu Gly Ala Gly Ile Thr Gly Tyr Asn Ser Asn
                125                 130                 135
TCT GCC GGT GCC ACA CTC GGT GTA GGC CTT GCT GCT GGT CTG GTG   450
Ser Ala Gly Ala Thr Leu Gly Val Gly Leu Ala Ala Gly Leu Val
                140                 145                 150
GGT ATG GCT GCA GAT GCG ATG GTG GAA GAT GTG AAC TAT ACC ATG   495
Gly Met Ala Ala Asp Ala Met Val Glu Asp Val Asn Tyr Thr Met
                155                 160                 165
ATC ACG GAT GTA CAG ATT GCA GAG CGT ACT AAG GCA ACG GTG ACA   540
Ile Thr Asp Val Gln Ile Ala Glu Arg Thr Lys Ala Thr Val Thr
                170                 175                 180
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ACG GAT AAT GTT GCC GCC CTG CGT CAG GGC ACA TCA GGT GCG AAA  585
Thr Asp Asn Val Ala Ala Leu Arg Gln Gly Thr Ser Gly Ala Lys
                185                 190                 195
ATT CAG ACC AGT ACT GAA ACA GGT AAC CAG CAT AAA TAC CAG ACC  630
Ile Gln Thr Ser Thr Glu Thr Gly Asn Gln His Lys Tyr Gln Thr
                200                 205                 210
CGT GTG GTT TCA AAT GCG AAC AAG GTT AAC CTG AAA TTT GAA GAG  675
Arg Val Val Ser Asn Ala Asn Lys Val Asn Leu Lys Phe Glu Glu
                215                 220                 225
GCG AAG CCT GTT CTC GAA GAC CAA CTG GCC AAA TCA ATC GCA AAT  720
Ala Lys Pro Val Leu Glu Asp Gln Leu Ala Lys Ser Ile Ala Asn
                230                 235                 240
ATT CTC TGA
Ile Leu CT
```

(2) INFORMATION FOR SEQ: ID NO: 17 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Amino acids 133-152 of the preS2 region of Hepatitis B virus

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Hepatitis B virus
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
5 10 15

Ser Gly Thr Val Cys
20

(2) INFORMATION FOR SEQ: ID NO: 18 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: Amino acids 734-754 of the transmembrane glycoprotein of HIV

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HIV
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Tyr Asp Arg Pro Glu Gly Ile Glu Glu Glu
5 10

Gly Gly Glu Arg Asp Arg Asp Arg Ser Gly Cys
15 20

(2) INFORMATION FOR SEQ: ID NO: 19 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: D1 T-cell epitope from Diphtheria toxoid with N and C terminal modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Corynebacterium diphtheriae
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = acetylalanine
At position 25, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Xaa Thr Asn Phe Val Glu Ser Ile Ile Asn
5 10

Leu Phe Gln Val Val His Asn Ser Tyr Asn
15 20

Arg Pro Ala Tyr Xaa
25

(2) INFORMATION FOR SEQ: ID NO: 20 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: D2 T-cell epitope from Diphtheria toxoid with N and C terminal modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Corynebacterium diphtheriae
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURE: At position 1, Xaa = acetylthreonine
At position 24, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Xaa Glu Pro Asn Leu His Asp Gly Tyr Ala
5 10

Val Ser Trp Asn Thr Val Glu Asp Ser Ile
15 20

Ile Arg Thr Xaa

(2) INFORMATION FOR SEQ: ID NO: 21 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: D3 T-cell epitope from Diphtheria toxoid with N and C terminal modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Corynebacterium diphtheriae
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURES: At position 1, Xaa = acetylaspartate
At position 23, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Xaa Ser Glu Thr Ala Asp Asn Leu Glu Lys
5 10

Thr Val Ala Ala Leu Ser Ile Leu Pro Gly
15 20

Ile Gly Xaa

(2) INFORMATION FOR SEQ: ID NO: 22 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: D4 T-cell epitope from Diphtheria toxoid with N and C terminal modification

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Modified Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Corynebacterium diphtheriae
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE:

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(ix) FEATURES: At position 39, Xaa = cysteinamide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met Val
5 10 15

Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe
20 25 30

Ala Ala Thr Asn Phe Val Glu Ser Xaa
35

(2) INFORMATION FOR SEQ: ID NO: 23 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: A sequence of the TraT protein of E coli predicted to be a T-cell epitope: TraT(T3)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Glu Ser Gln Gly Trp Leu Asn Arg Gly Tyr Glu Gly Ala Ala Val
5 10 15

Gly Ala Ala Leu Gly Ala Gly Ile Thr Gly
20 25

(2) INFORMATION FOR SEQ: ID NO: 24 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: A sequence of the TraT protein of E coli predicted to be a T-cell epitope: TraT(T6)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ser Thr Glu Thr Gly Asn Gln His Lys Tyr Gln Thr Arg Val Val
5 10 15

Ser Asn Ala Asn Lys
20

(2) INFORMATION FOR SEQ: ID NO: 25 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 Amino acids
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide
(A) DESCRIPTION: A sequence of the TraT protein of E coli predicted to be a T-cell epitope: TraT(T7)

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: E coli
(B) STRAIN:
(C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE:
(E) HAPLOTYPE:
(F) TISSUE TYPE:
(G) CELL TYPE:
(H) CELL LINE:
(I) ORGANELLE:

(vii) IMMEDIATE SOURCE:
(A) LIBRARY:
(B) CLONE: BTA 1349

(viii) POSITION IN GENOME:
(A) CHROMOSOME/SEGMENT:
(B) MAP POSITION:
(C) UNITS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Lys Val Asn Leu Lys Phe Glu Glu Ala Lys
5 10

Pro Val Leu Glu Asp Gln Leu Ala Lys
15

CLAIMS

1. A T-cell epitope, comprising a portion of the amino acid sequence of the protein TraT.

2. The T-cell epitope:
GlyAlaMetSerThrAlaIleLysLysArgAsnLeuGluValLysThrGln MetSerGluThrIleTrpLeuGlu.

3. The T-cell epitope:
GlyLeuGlnGlyLysIleAlaAspAlaValLysAlaLysGly.

4. The T-cell epitope:
GlyLeuAlaAlaGlyLeuValGlyMetAlaAlaAspAlaMetValGluAsp ValAsn.

5. The T-cell epitope:
SerThrGluThrGlyAsnGlnHisHisTyrGlnThrArgValValSerAsn AlaAsnLys.

6. The T-cell epitope:
SerThrGluThrGlyAsnGlnHisLysTyrGlnThrArgValValSerAsnAla AsnLys.

7. A T-cell epitope according to any one of claims 1 to 6 wherein the amino acid sequence of the T-cell epitope is modified.

8. A T-cell epitope according to claim 7 comprising an additional N-terminal residue or a modified N-terminal residue such as an N-terminal pyro-glutamic acid residue.

9. A T-cell epitope according to claim 7 or claim 8 comprising an additional or modified C-terminal residue, such as a C-terminal cysteinamide residue.

10. A complex comprising at least one T-cell epitope according to any one of claims 1 to 9, linked to at least one immunogen, such that the at least one T-cell epitope maintains its function as a T-cell epitope and the at least one immunogen presents at least one antigenic determinant against which an immune response can be raised.

11. A complex according to claim 10 wherein the at least one immunogen is selected from the group consisting of: the circumsporozoite surface protein of Plasmodium falciparum, the synthetic immunogen NH_2 Cys (Asn Pro Asn

Ala)$_4$ derived from the circumsporozoite surface protein of Plasmodium falciparum, all or part of luteinizing hormone or somatostatin, and immunogenic proteins which are all or part of: the S protein of hepatitis B virus, the AIDS virus, influenza virus, foot and mouth disease virus, inhibin or FSH.

12. A vaccine comprising a complex according to claim 10 or 11 together with a pharmaceutically acceptable carrier, excipient, diluent and/or adjuvant.

13. A hybrid polynucleotide molecule which consists of: a polynucleotide sequence which acts as a coding sequence for at least one T-cell epitope according to any one of claims 1 to 9, fused to a polynucleotide sequence which acts as a coding sequence for at least one immunogen.

14. A hybrid polynucleotide molecule which consists of: a polynucleotide sequence which acts as a coding sequence for at least one immunogen, into which is inserted at least one polynucleotide sequence which acts as a coding sequence for a T-cell epitope according to any one of claims 1 to 7.

15. A hybrid polynucleotide molecule which consists of: a first polynucleotide sequence which acts as a coding sequence for all or part of the TraT molecule, with a polynucleotide sequence which acts as a coding sequence for at least one immunogen inserted into the first polynucleotide sequence, adjacent to at least one T-cell epitope according to any one of claims 1 to 6.

16. A hybrid polynucleotide molecule according to any one of claims 13 to 15 which molecule is a DNA molecule.

17. A hybrid DNA molecule according to claim 16 wherein the resulting fusion protein is exported to and exposed on the host cell surface.

18. A fused gene comprising a hybrid DNA sequence according to claim 16 or 17 fused to a portable promoter, such as the P_L promoter of the bacteriophage lambda.

19. A recombinant DNA molecule comprising a DNA sequence according to claim 16 or 17 and vector DNA.

20. A recombinant DNA molecule according to claim 19 which includes an expression control sequence operatively linked to the DNA sequence.

21. A transformant host, carrying the genetic information for the biosynthesis of a complex according to claim 10 or 11.

22. A transformant host according to claim 21, wherein the complex is expressed on the cell surface of the transformant host.

23. An expression product of a transformant host according to claim 21 or 22, comprising a complex according to claim 10 or 11.

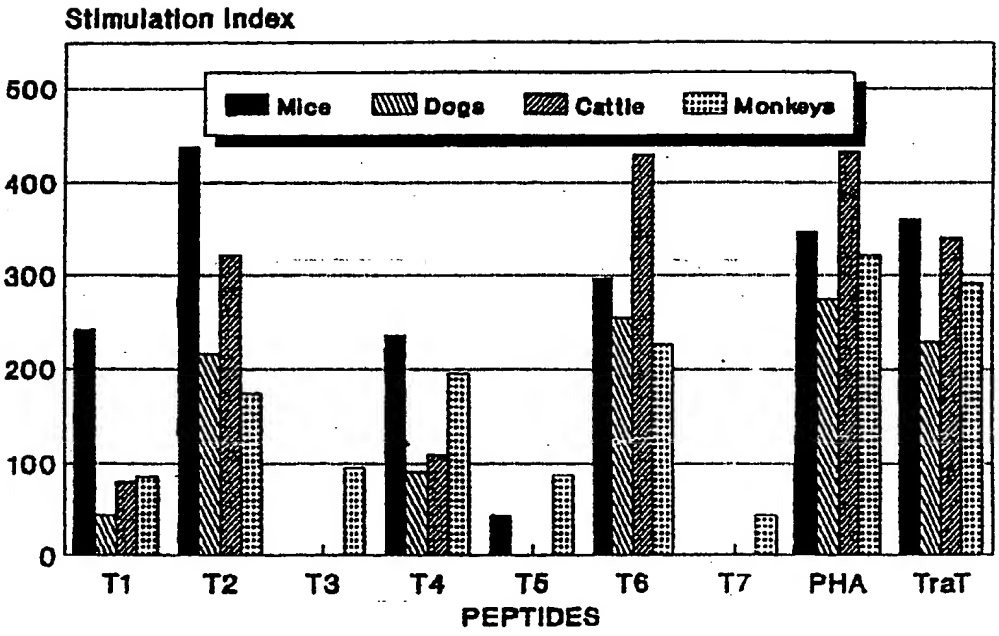
Stimulation Index
500
400
300
200
100
0
Mice
Dogs
Cattle
Monkeys
T1
T2
T3
T4
T5
T6
T7
PHA
TraT
PEPTIDES

FIGURE 1

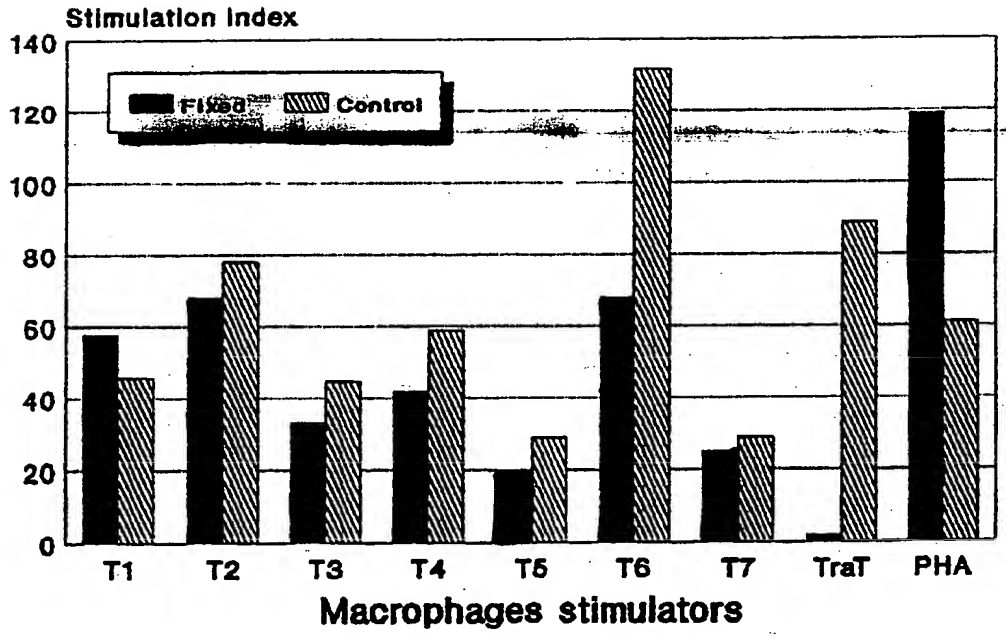
Stimulation Index
140
120
100
80
60
40
20
0
Fixed
Control
T1
T2
T3
T4
T5
T6
T7
TraT
PHA
Macrophages stimulators

FIGURE 2

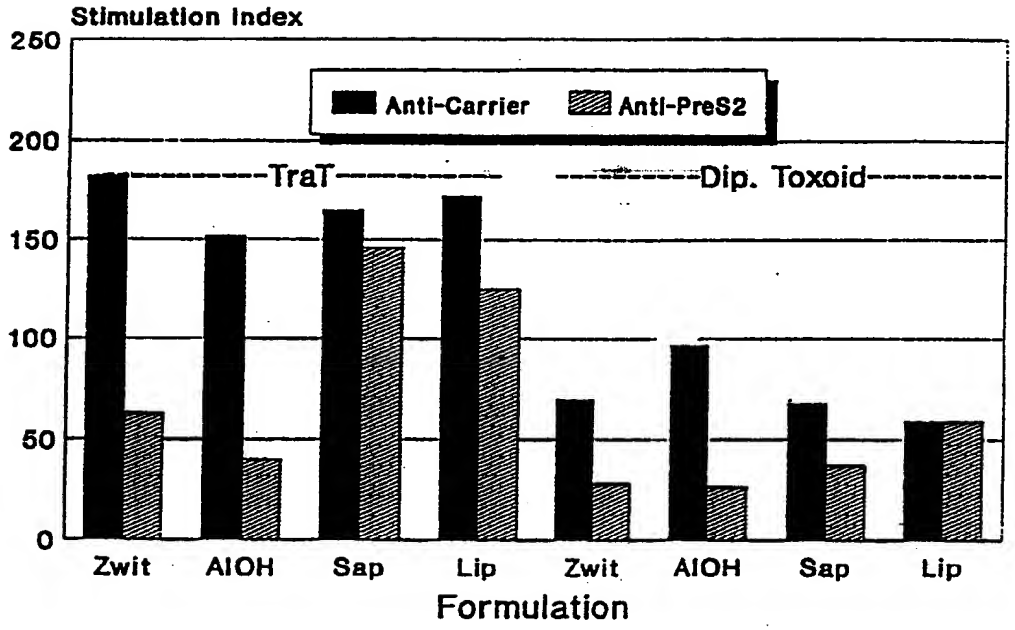
Stimulation Index
250
200
150
100
50
0
Anti-Carrier
Anti-PreS2
TraT
Dip. Toxoid
Zwit
AlOH
Sap
Lip
Zwit
AlOH
Sap
Lip
Formulation

FIGURE 3

FIGURE 4

Signal Sequence

```
                                                                                                    25
ATG AAA AAA TTG ATG ATG GTT GCA CTG GTC AGT TCC ACT CTG GCC CTT TCA GGC TGT GGT GCG ATG AGC ACA GCA
Met Lys Lys Leu Met Met Val Ala Leu Val Ser Ser Thr Leu Ala Leu Ser Gly Cys Gly Ala Met Ser Thr Ala

                                                                                                    50
ATC AAG AAG CGT AAC CTT GAG GTG AAG ACT CAG ATG AGT GAG ACC ATC TGG CTT GAA CCC GCC AGC GAA CGC
Ile Lys Lys Arg Asn Leu Glu Val Lys Thr Gln Met Ser Glu Thr Ile Trp Leu Glu Pro Ala Ser Glu Arg
                                T1

                                                                                                    75
ACG GTA TTT CTG CAG ATC AAA AAC ACG TCT GAT AAA GAC ATG AGT GGG CTG CAG GGC AAA ATT GCT GAT GCT GTG
Thr Val Phe Leu Gln Ile Lys Asn Thr Ser Asp Lys Asp Met Ser Gly Leu Gln Gly Lys Ile Ala Asp Ala Val
                                                                T2
                                                                                                   100
AAA GCA AAA GGA TAT CAG GTG GTG ACT TCT CCG GAT AAA GCC TAC TAC TGG ATT CAG GCG AAT GTG CTG AAG GCC
Lys Ala Lys Gly Tyr Gln Val Val Thr Ser Pro Asp Lys Ala Tyr Tyr Trp Ile Gln Ala Asn Val Leu Lys Ala

                                                                                                   125
GAT AAG ATG GAT CTG CGG GAG TCT CAG GGA TGG CTG AAC CGT GGT TAT GAA GGC GCA GCA GTT GGT GCA GCG TTA
Asp Lys Met Asp Leu Arg Glu Ser Gln Gly Trp Leu Asn Arg Gly Tyr Glu Gly Ala Ala Val Gly Ala Ala Leu
                                                        T3
                                                                                                   150
GGT GCC GGT ATT ACC GGC TAT AAC TCA AAT TCT GCC GGT GCC ACA CTC GGT GTA GGC CTT GCT GCT GGT CTG GTG
Gly Ala Gly Ile Thr Gly Tyr Asn Ser Asn Ser Ala Gly Ala Thr Leu Gly Val Gly Leu Ala Ala Gly Leu Val

                                                                                                   175
GGT ATG GCT GCA GAT GCG ATG GTG GAA GAT GTG AAC TAT ACC ATG ATC ACG GAT GTA CAG ATT GCA GAG CGT ACT
Gly Met Ala Ala Asp Ala Met Val Glu Asp Val Asn Tyr Thr Met Ile Thr Asp Val Gln Ile Ala Glu Arg Thr
          T4
                                                                                                   200
AAG GCA ACG GTG ACA ACG GAT AAT GTT GCC GCC CTG CGT CAG GGC ACA TCA GGT GCG AAA ATT CAG ACC AGT ACT
Lys Ala Thr Val Thr Thr Asp Asn Val Ala Ala Leu Arg Gln Gly Thr Ser Gly Ala Lys Ile Gln Thr Ser Thr
                T5
                                                                                                   225
GAA ACA GGT AAC CAG CAT AAA TAC CAG ACC CGT GTG GTT TCA AAT GCG AAC AAG GTT AAC CTG AAA TTT GAA GAG
Glu Thr Gly Asn Gln His Lys Tyr Gln Thr Arg Val Val Ser Asn Ala Asn Lys Val Asn Leu Lys Phe Glu Glu
                T6

GCG AAG CCT GTT CTC GAA GAC CAA CTG GCC AAA TCA ATC GCA AAT ATT CTC TGA
Ala Lys Pro Val Leu Glu Asp Gln Leu Ala Lys Ser Ile Ala Asn Ile Leu CT
          T7
```

FIGURE 5

INTERNATIONAL SEARCH REPORT

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)[6]

According to International Patent classification (IPC) or to both National Classification and IPC

Int. Cl.[5] C07K 13/00, 7/08, 7/10, 15/12, 15/04, 15/16, C12N 15/31, 15/62, A61K 39/02, 39/385, 39/108.

II. FIELDS SEARCHED

Minimum Documentation Searched [7]

Classification System	Classification Symbols
	DERWENT WPI/WPIL; CHEMICAL ABSTRACTS KEYWORDS: [(E() COLI OR ESCHERICHIA COLI) AND (MEMBRANE# OR T() CELL OR LYMPHOCYTE#)] OR TRAT.

Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched [8]

CHEMICAL ABSTRACTS: STN CAS-ONLINE PROTEIN SEQUENCE SEARCH

AU: C07K 7/08, 7/10, 13/00, 15/04, 15/16, C07C 103/52, C07G 7/00.

III. DOCUMENTS CONSIDERED TO BE RELEVANT [9]

Category[9]	Citation of Document, [11] with indication, where appropriate of the relevant passages [12]	Relevant to Claim No [13]
X	Dissertation Abstracts International vol. 46, no. 5, November 1985 (PERUMAL, NARAYANAN BHAGAVATI), "Biochemical Characterization of the F Sex Factor traT surface exclusion gene product".	(1, 7, 10, 13-16, 19, 20)
X	Molecular and General Genetics, (1987) vol. 210:pages178-180 (SOILA SUKUPOLVI et al.), "Amino acid alterations in a hydrophobic region of the TraT protein of R6-5 increase the outer membrane permeability of enteric bacteria".	(1)
	(continued)	

[9] Special categories of cited documents : [10]

"A" Document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior t the international filing date but later than the priority date claimed

"T" Later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
20 December 1991 (20.12.91)	3 January 92
International Searching Authority	Signature of Authorized Officer
AUSTRALIAN PATENT OFFICE	N.F. BLOM

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category*	Citation of Document, [11] with indication, where appropriate of the relevant passages [12]	Relevant to Claim No [13]
X	Molecular Microbiology (1990) 4(1) pages 49-57 (S. SUKUPOLVI et al.), "Characterization of the traT gene and mutants that increase outer membrane permeability from the Salmonella typhimurium virulence plasmid". (in particular pages 50, 51).	(1, 15, 16, 18-23)
X	Molecular Microbiology (1990) 4(8), pages 1259-1268 (I.M. TAYLOR et al.), "The TraT lipoprotein as a vehicle for the transport of foreign antigenic determinants to the cell surface of Escherichia coli K12:structure-function relationships in the TraT protein".	(1, 7-23)
P, X	Microbiological Reviews, Dec. 1990, vol 54, no. 4, pages 331-341 (SOILA SUKUPOLVI et al.) "TraT Lipoprotein, a plasmid-specified mediator of interactions between gram-negative bacteria and their environment".	(1, 7, 10, 12, 14, 15, 18-23)
P, X	The Journal of Immunology, vol 146, no 3, pages 793-798, Feb. 1, 1991, (S. CROFT et al.) "TraT: A powerful carrier molecule for the stimulation of immune responses to protein and peptide antigens".	(1, 7, 9-11)
X	AU, A, 73510/87 (BIOENTERPRISES PTY. LTD) 5 November 1987 (05.11.87)	(1, 7, 9-23)
X	AU, A, 43360/89 (BIOTECHNOLOGY AUSTRALIA PTY. LTD) 5 April 1990 (05.04.90)	(1, 7, 10, 12-23)
A	AU, A, 30654/89 (PRAXIS BIOLOGICS, INC.) 10 August 1989 (10.08.89)	(1, 7, 10, 12-23)
A	AU, A, 35046/89 (F. HOFFMANN-LA ROCHE & CO. AKTIENGESELLSCHAFT), 30 November 1989 (30.11.89)	(1, 7, 10, 12-23)

ANNEX TO THE INTERNATIONAL SEARCH REPORT ON INTERNATIONAL APPLICATION NO. PCT/AU 91/00429

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report	Patent Family Member		
AU 43360/89	EP 391997	JP 3503054	WO 9003433
AU 30654/89	DK 1829/90	EP 399001	FI 903292
	JP 3502691	NO 902909	WO 8906974
AU 35046/89	DK 2505/89	EP 343460	GB 8812214
	JP 2042099	ZA 8903702	
AU 73510/87	CN 87103784	DK 6679/87	EP 267204
	JP 1500117	KR 9102693	NZ 220027
	IL 82235	WO 8706590	ZA 8702795